

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:08:53 ; Search time 19.81 Seconds
(without alignments)
236.905 Million cell updates/sec

Title: US-09-772-103-8
Perfect score: 655
Sequence: 1 MDPQVQIFSLISAVILS.....CQWSSYPLTFGGTKVEIK 128

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

all number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	446	68.1	129	1	P01680 mus musculus
2	444.5	67.9	108	1	KV1P_MOUSE
3	441.5	67.4	108	1	KV1V_HUMAN
4	436.5	66.6	108	1	KV1O_HUMAN
5	435.5	66.5	108	1	KV1B_HUMAN
6	434.5	66.3	108	1	KV1Y_HUMAN
7	432.5	66.0	108	1	KV1H_HUMAN
8	431	65.8	109	1	KV1I_HUMAN
9	430.5	65.7	129	1	KV1X_HUMAN
10	427.5	65.3	108	1	KV1S_HUMAN
11	427.5	65.3	129	1	KV1W_HUMAN
12	422.5	64.5	108	1	KV1F_HUMAN
13	422.5	64.5	108	1	KV1M_HUMAN
14	421.5	64.4	108	1	KV1G_HUMAN
15	421.5	64.4	108	1	KV1J_HUMAN
16	420.5	64.2	108	1	KV1A_HUMAN
17	418.5	63.9	108	1	KV1D_HUMAN
18	416	63.5	107	1	KV1L_HUMAN
19	413.5	63.1	108	1	KV1K_HUMAN
20	412.5	63.0	108	1	KV1E_HUMAN
21	412.5	63.0	108	1	KV1N_HUMAN
22	412	62.9	108	1	KV6K_MOUSE
23	409.5	62.5	108	1	KV1Q_HUMAN
24	408.5	62.4	108	1	KV1C_HUMAN
25	408.5	62.4	108	1	KV5J_MOUSE
26	408.5	62.4	117	1	KV1J_HUMAN
27	401.5	61.3	117	1	KV1I_HUMAN
28	399	60.9	107	1	KV6F_MOUSE
29	398.5	60.8	112	1	KV1U_HUMAN
30	394	60.2	107	1	KV6I_MOUSE
31	393	60.0	107	1	KV6H_MOUSE
32	393	60.0	107	1	KV6J_MOUSE
33	392	59.8	107	1	KV6J_MOUSE

34	389	59.4	133	1	KV4B_HUMAN
35	388.5	59.3	108	1	KV5K_MOUSE
36	388.5	59.3	134	1	KV4C_HUMAN
37	386.5	59.0	136	1	KV5B_MOUSE
38	385.5	58.9	108	1	KV5Q_MOUSE
39	384	58.6	129	1	KV3L_HUMAN
40	383.5	58.5	108	1	KV5L_MOUSE
41	383.5	58.5	108	1	KV5M_MOUSE
42	383.5	58.5	108	1	KV5N_MOUSE
43	383.5	58.5	149	1	KV3M_HUMAN
44	381	58.2	129	1	KV3M_HUMAN
45	379	57.9	107	1	KV6A_MOUSE

ALIGNMENTS

RESULT 1
KV4A_MOUSE
ID KV4A_MOUSE STANDARD; PRT; 129 AA.
AC P01680:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-IV REGION S107B PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=82115300; PubMed=6799208;
KW Kwan S.-P., Max E.E., Seidman J.G., Leder P., Scharff M.D.;
RL Cell 26:57-66(1981).
CC -1- MISCELLANEOUS: THIS PROTEIN, IN WHICH THERE IS A DELETION OF TWO
AMINO ACIDS AT THE V-J RECOMBINATION SITE (AFTER POSITION 118), IS
SYNTHESIZED BUT NOT SECRETED IN CELLS THAT EXPRESS AND SECRETE THE
NORMAL KAPPA CHAIN S107.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00577; AAA38780.1; -;
CC EMBL; V00780; CAA24157.1; -;
CC PIR; A01943; KVM57B.
CC HSP; P01679; 2FBT.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IgV; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 22
CC CHAIN 23 129
CC DOMAIN 23 45
CC DOMAIN 23 45
CC DOMAIN 46 57
CC DOMAIN 58 72
CC DOMAIN 73 79
CC DOMAIN 80 111
CC DOMAIN 112 118
CC DOMAIN 119 128
CC DISULFID 45 111
CC NON_TER 129 129
CC SEQUENCE 129 AA; 13833 MW; E4BB73072DCF6BE4 CRC64;
SQ

Query Match 68.1%; Score 446; DB 1; Length 129;
Best Local Similarity 66.9%; Pred. No. 3.5e-36;

us-09-772-103-8.rsp

Mon Jul 1 16:28:15 2002

Matches 87; Conservative 21; Mismatches 18; Indels 4; Gaps 2;

QY 1 MFOVQIFELLISAVILSRGDIQWQSPSSLSASVGRVTITCSATSSI--TYMSWYQ 58
 DB 1 MDLQVQIIFLLISVIMSRGENVLIFQSPAINAASIGQKVTMTCSASSSVSSVHLHWYQ 60
 QY 59 QKPKAPKLLIYDTSNLASGVPSRFGSGSGTDTYITLTISSLPQEDFATYCCQWSSYPLT 118
 DB 61 QKSGASPLHRLHRSNLASGVPSRFGSGSGTDTYITLTISSVVEADDATYCCQWSSYPLT 118
 QY 119 FGGTKVEIK 128
 DB 119 FGSQTKLEIK 128

RESULT 2
 ID KVLP_HUMAN STANDARD; PRT; 108 AA.
 AC P01608;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-I REGION ROY.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=68362076; PubMed=5595110;
 RA Hilschmann N.;
 RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and Cum.)";
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
 RN [2]
 RP REVISIONS TO 39 AND 41.
 RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
 RA Steinhilber-Kayne M., Suter L., Watanabe S.;
 RL (In) Franek F., Shugar D. (eds.);
 RL Gamma globulins: structure and function, pp.57-74, Academic Press,
 RL New York (1969).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
 CC MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
 CC PIR; A01874; K1HURY.
 DR HSP; P80362; 1WTL.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IgV; 1.
 KW Immunoglobulin v region; Bence-Jones protein.
 FT DOMAIN 1 23
 FT DOMAIN 2 34
 FT DOMAIN 3 49
 FT DOMAIN 4 56
 FT DOMAIN 5 88
 FT DOMAIN 6 97
 FT DOMAIN 7 107
 FT DISULFID 23 88
 FT NON_TER 108
 SQ SEQUENCE 108 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;

Query Match 67.9%; Score 444.5; DB 1; Length 108;
 Best Local Similarity 78.5%; Pred. No. 4e-36;
 Matches 84; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

QY 23 DIQMTQSPSSLSASVGRVTITCSATSSI--TYMSWYQKPKAPKLLIYDTSNLASGVPS 81
 DB 1 DIQMTQSPSSLSASVGRVTITCSATSSI--TYMSWYQKPKAPKLLIYDTSNLASGVPS 60
 QY 82 RFGSGSGTDTYITLTISSLPQEDFATYCCQWSSYPLTGGTKVEIK 128

DB 61 RFGSGSGTDTYITLTISSLPQEDFATYCCQWSSYPLTGGTKVEIK 107

RESULT 3
 ID KVIV_HUMAN STANDARD; PRT; 108 AA.
 AC P04430;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-I REGION BAN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=86174817; PubMed=3083240;
 RA Dwulet F.E., O'Connor T.P., Benson M.D.;
 RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
 RL Mol. Immunol. 23:73-78(1986).
 DR PIR; A01878; K1HUBN.
 DR HSP; P80362; 1WTL.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IgV; 1.
 KW Immunoglobulin v region; Amyloid.
 FT DOMAIN 1 23
 FT DOMAIN 2 34
 FT DOMAIN 3 49
 FT DOMAIN 4 56
 FT DOMAIN 5 88
 FT DOMAIN 6 97
 FT DOMAIN 7 107
 FT DISULFID 23 88
 FT NON_TER 108
 SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 67.4%; Score 441.5; DB 1; Length 108;
 Best Local Similarity 78.5%; Pred. No. 7.7e-36;
 Matches 84; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

QY 23 DIQMTQSPSSLSASVGRVTITCSATSSI--TYMSWYQKPKAPKLLIYDTSNLASGVPS 81
 DB 1 DIQMTQSPSSLSASVGRVTITCSATSSI--TYMSWYQKPKAPKLLIYDTSNLASGVPS 60
 QY 82 RFGSGSGTDTYITLTISSLPQEDFATYCCQWSSYPLTGGTKVEIK 128
 DB 61 NFGSGSGTDTYITLTISSLPQEDFATYCCQWSSYPLTGGTKVEIK 107

RESULT 4
 ID KVIO_HUMAN STANDARD; PRT; 108 AA.
 AC P01607;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-I REGION REI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=76023758; PubMed=809329;
 RA Palm W., Hilschmann N.;
 RT "The primary structure of a crystalline monoclonal immunoglobulin kappa-type L-chain, subgroup I (Bence-Jones protein Re.). isolation and characterization of the tryptic peptides; the complete amino acid sequence of the protein; a contribution to the elucidation of the

three-dimensional structure of antibodies, in particular their
 Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
 [2]
 X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 MEDLINE-76039968; PubMed-1182131;
 Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
 "The molecular structure of a dimer composed of the variable portions
 of the Bence-Jones protein REI refined at 2.0-A resolution.";
 Biochemistry 14:4943-4952(1975).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
 MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01873; KIHUE.
 DR PDB; 1REI; 17-FEB-84.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Ig; 1.
 Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 DOMAIN 1 23
 FRAMEWORK 1.
 FT DOMAIN 24 34
 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 35 49
 FRAMEWORK 2.
 FT DOMAIN 50 56
 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 57 88
 FRAMEWORK 3.
 FT DOMAIN 89 97
 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 98 107
 FRAMEWORK 4.
 FT DISULFID 23 88
 FT STRAND 4 7
 FT STRAND 10 13
 FT TURN 15 16
 FT STRAND 19 25
 FT TURN 30 31
 FT STRAND 33 38
 FT TURN 40 41
 FT STRAND 45 49
 FT TURN 50 52
 FT STRAND 53 54
 FT TURN 56 57
 FT STRAND 60 61
 FT TURN 62 67
 FT STRAND 68 69
 FT TURN 70 75
 FT HELIX 80 82
 FT STRAND 85 90
 FT TURN 98 98
 FT STRAND 102 106
 FT NON_TER 108 108
 SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Query Match 66.6%; Score 436.5; DB 1; Length 108;
 Best Local Similarity 79.2%; Pred. No. 2.3e-35;
 Matches 84; Conservative 8; Mismatches 13; Indels 1; Gaps 1;
 QY 23 DIQMTQSPSSLSASVGDRTVITCSATSS-ITVMSYQKPGKAPKLLIYDTSNLSAGVPS 81
 DB 1 DIQMTQSPSSLSASVGDRTVITCSATSS-ITVMSYQKPGKAPKLLIYDTSNLSAGVPS 81
 QY 82 RFGSGSGTDYTLTISSLQPEDFATYYCQWSSYPLTFGGTKVEIK 127
 DB 61 RFGSGSGTDYTLTISSLQPEDFATYYCQWSSYPLTFGGTKVEIK 127
 RESULT 5
 KVIB_HUMAN STANDARD; PRT; 108 AA.
 ID KVIB_HUMAN
 AC P01594;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE IG KAPPA CHAIN V-I REGION AU.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1] TaxID=9606;
 RP SEQUENCE.
 RX MEDLINE-72189444; PubMed-5028201;
 RA Schiechl H., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
 protein Au).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE-77022433; PubMed-1234024;
 RA Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
 RA Schwager P., Steigemann W., Schramm H.J.;
 RT "The structure determination of the variable portion of the
 Bence-Jones protein Au.";
 RL Biophys. Struct. Mech. 1:139-146(1975).
 CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
 MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
 REGION OF THE KAPPA CHAIN REI.
 CC -1- MISCELLANEOUS: THIS C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01862; KIHUAU.
 DR HSSP; P01607; 1REI.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Ig; 1.
 Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23
 FRAMEWORK 1.
 FT DOMAIN 24 34
 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 35 49
 FRAMEWORK 2.
 FT DOMAIN 50 56
 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 57 88
 FRAMEWORK 3.
 FT DOMAIN 89 97
 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 98 107
 FRAMEWORK 4.
 FT DISULFID 23 88
 FT NON_TER 108 108
 SEQUENCE 108 AA; 11939 MW; E8011187E6F6FB9 CRC64;

Query Match 66.5%; Score 435.5; DB 1; Length 108;
 Best Local Similarity 79.4%; Pred. No. 2.9e-35;
 Matches 85; Conservative 6; Mismatches 15; Indels 1; Gaps 1;
 QY 23 DIQMTQSPSSLSASVGDRTVITCSATSSIT-YMSYQKPGKAPKLLIYDTSNLSAGVPS 81
 DB 1 DIQMTQSPSSLSASVGDRTVITCSATSSIT-YMSYQKPGKAPKLLIYDTSNLSAGVPS 81
 QY 82 RFGSGSGTDYTLTISSLQPEDFATYYCQWSSYPLTFGGTKVEIK 128
 DB 61 RFGSGSGTDYTLTISSLQPEDFATYYCQWSSYPLTFGGTKVEIK 128
 RESULT 6
 KVIL_HUMAN STANDARD; PRT; 108 AA.
 ID KVIL_HUMAN
 AC P80362;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-I REGION WAT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1] TaxID=9606;
 RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE-95086080; PubMed-7993911;
 RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
 RA Solomon A., Stevens F.J., Schiffer M.,

^aComparison of crystal structures of two homologous proteins: structural origin of altered domain interactions in immunoglobulin light-chain dimers.⁶ *Cell*, 77, 1484-1485 (1994).

[2]
SEQUENCE OF 1-35; PubMed=6167731;
MEDLINE=81297384; PubMed=6167731;
Stevens F.J., Westholm F.A., Pangiotopoulos N., Schiffer M.,
RA
RA
RA
Poppe R.A., Solomon A.;
RA "Characterization and preliminary crystallographic data on the VL-
RA related fragment of the human XI Bence Jones protein wat.";
RL J. Mol. Biol. 147:185-193(1981); BENCE-JONES PROTEIN.
RL

CC -1- MISCELLANEOUS: THIS IS A BENCE JONES PROTEIN.
DR PDB: 1WTL; 01-NOV-94.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR InterPro: IPR000047; Ig_1.
DR Pfam: PF00046; IGV; 1.
DR SMART: SM00406; IGV; 1.
DR Conserved: 2D-structure.

KR		Immunoglobulin V region; Bence-Jones protein; 3D structure.
DW	1	FRAMEWORK 1.
FT	23	FRAMEWORK 1.
FT	24	COMPLEMENTARITY-DETERMINING 1.
FT	25	FRAMEWORK 2.
FT	35	FRAMEWORK 2.
FT	49	COMPLEMENTARITY-DETERMINING 2.
FT	56	COMPLEMENTARITY-DETERMINING 2.
FT	57	FRAMEWORK 3
FT	88	COMPLEMENTARITY-DETERMINING 3.
FT	89	COMPLEMENTARITY-DETERMINING 3.
FT	97	FRAMEWORK 4.
FT	98	COMPLEMENTARITY-DETERMINING 4.
FT	107	FRAMEWORK 4.
FT	23	BY SIMILARITY.
FT	88	BY SIMILARITY.
FT	CONFLICT	TN -> SD (IN REF. 2).
FT	30	
FT	31	
FT	108	
FT	NON_TER	
FT	SEQUENCE	
FC	108 AA;	D9D941B3F0FAE597 CRC64;
FC	108 AA;	11737 MW;

Query Match	66.3%;	Score 434.5;	DB 1;	Length 108;
Best Local Similarity	77.6%;	Pred. No. 3.6e-35;		
Matches 83;	Conservative 12;	Mismatches 11;	Indels 1;	Gaps 1;

Matches	83: Conservation
QY	23 DIQMTQSPSSLSASVGRVTITCSATSSIT-YMSWYQKQKQKAPKLLIYDTSNLASGVPS 81
DB	1 DIQMTQSPSSLSASVGRVTITCSASODITNYVNFQQRQAPKVLIIYGASILETVPS 60
QY	82 RFSGSGSGTDYTLTIISLPEDFAFYHQQQWSVPLTFGGGTVEIK 128
DB	82 RFSGSGSGTDYTLTIISLPEDFAFYHQQQWSVPLTFGGGTVEIK 107

RESULT	7	STANDARD	PRT	108 AA.
KV1H_HUMAN				
10	PO1600; 1986 (Rel. 01, Created)			
21-JUL-1986	(Rel. 01, Last sequence update)			
DT	21-JUL-1986 (Rel. 38, Last annotation update)			
DI	15-JUL-1993 (Rel. 38, Last annotation update)			
DE	IG KAPPA CHAIN V-I REGION HAU.			
OS	homo sapiens (human)			
OC	Karyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=71032830; PubMed=4097974;			
RA	Watanabe S., Hilschmann N.;			
RT	"The primary structure of a monoclonal kappa-type immunoglobulin L-			
RT	chain of subgroup I (Bence-Jones Protein Hau): subdivision within			
RT	supergroups."			
RT				
RT				

RT subgroups.²⁰
 RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
 CC - MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC - MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 CC PIR: A01868; K1HUHU.
 DR HSP: P80362; 1WTL.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.

Immunoglobulin V region; Bence-Jones protein.
KW
DOMAIN 1
FT 23
DOMAIN 2
FT 34
DOMAIN 3
FT 49
DOMAIN 4
FT 56
DOMAIN 5
FT 87
DOMAIN 6
FT 97
DOMAIN 7
FT 107
DOMAIN 8
FT 108
DISULFID
NON_TER
SEQUENCE
SQ

[illegible]

Db	I	DIQMUSPSEKAVYER	
Qy	82	RFSGSGDTYLTISLQPEDFAYYCOQSSYPLTFGGTKVEIK	128
		: : :	
	61	RFSGSGDTYLTISLQPEDFAYYCOQNYLTPTSGGQTRVEIK	107

	RESULT	8		STANDARD;	PRT;	109 AA.
ID	KVIT_HUMAN		KVIT_HUMAN			
AC	P01612;	1986	(Rel. 01, Created)			
DT	21-JUL-1986	(Rel. 01, Last sequence update)				
DT	21-JUL-1986	(Rel. 01, Last annotation update)				
DT	15-JUL-1999	(Rel. 38, Last annotation update)				
DT	15-JUL-1999	(IN V.I. REGION MEV.)				

DE	IG KAPPA CHAIN
OS	Homo sapiens (Human)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE.
RX	Medlitz M., Linke R.P.; EDLITZ-83081018; PubMed=6816713; "Primary structure of the variable part of an amyloidogenic Bence-Jones protein (Mev). An unusual insertion in the third hypervariable region of a human kappa-immunoglobulin light chain."; Hoppe-Seyler's Z. Physiol. Chem. 363:1347-1358(1982).
CC	-I- MISCELLANEOUS: ANOTHER FORM THAT LACKED RESIDUES 1-3 WAS ALSO FOUND.

CC	-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A REDUCED	
DR	PIR; A01879; K1HUMV.	
DR	HSP; P80362; LWTL.	
DR	InterPro; IPR003006; Ig_MHC.	
DR	InterPro; IPR003596; Ig_V.	
DR	Pfam; PF00047; Ig; 1.	
DR	SMART; SM00406; IgV; 1.	
KW	Immunoglobulin V region.	
FT	DOMAIN 1	23
FT	DOMAIN 24	34
FT	DOMAIN 35	49
FT	DOMAIN 50	56
FT	DOMAIN 57	88
FT	DOMAIN 89	98
FT	DOMAIN 99	108
FT	DISULFID 23	88
FT	NON_TER	109
FO	SEQUENCE 109 AA; 11870 MW; B6ABF451D5D55F5A0 CRC64;	

Query Match	65.8%	Score	431;	DB 1;	Length	109,
Best Local Similarity	78.7%	Pred. No.	8+35;			
Matches	85;	Mismatches	11;	Indels	2;	Gaps
		Conservative				

23 DIQMTQSPSSLASVGDRVTITCSAT-SSITYMSWYQQKPGKAPKLLIDISNLRGCT

us-09-772-103-8-rsp

Db 1 DVQMTQSPSSLSASVGRVITTCRASQSSVDYLNWYQKPKAPKLLIFDTSNLQSGVPS 60
 QY 82 RFGSGSGTDYTLTISSLPEDFATYYCQOWSSYP-LTFGGGKVEIK 128
 Db 61 RFGSGRSGTDFTLTISLQPDFAFYCQSYTNPFTVFGGTTVDIK 108

RESULT 9
 ID KVIS_HUMAN STANDARD; PRT; 129 AA.
 AC P04432;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DE IG KAPPA CHAIN V-I REGION DAUDI PRECURSOR.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]

SEQUENCE FROM N.A.
 MEDLINE=85014148; PubMed=6091049;
 Klobbeck H.G., Combriato G., Zachau H.G.;
 "Immunoglobulin genes of the kappa light chain type from two human
 lymphoid cell lines are closely related.";
 Nucleic Acids Res. 12:6995-7006(1984).
 CC -----

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 entities requires a license agreement. Usage by and for commercial
 or send an email to license@lsb-sib.ch)

EMBL; X00966; CAA25478.1; ALT_TERM.
 DR PIR: A01884; KIHUJ.
 DR HSP: P80362; IWT.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_v.
 DR SMART: SM00406; Ig; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION DAUDI.
 FT DOMAIN 23 45 FRAMEWORK 1.
 FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 57 71 FRAMEWORK 2.
 FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 79 110 FRAMEWORK 3.
 FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 120 129 FRAMEWORK 4.
 FT DISULFID 45 110 BY SIMILARITY.
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 14235 MW; CAF076BC7E5574C8 CRC64;

Query Match 65.7%; Score 430.5; DB 1; Length 129;
 Best Local Similarity 69.5%; Pred. No. 1.1e-34;
 Matches 91; Conservative 12; Mismatches 23; Indels 5; Gaps 3;

QY 1 MDOFV--QIFSFLLISASVILSGDIQMTQSPSSLSASVGRVITTCRASQSSVDYLNWYQKPKAPKLLIFDTSNLQSGVPS 3;
 Db 1 MDMRPAQLGLLLWLRLV--KCDIQMTQSPSSLSASVGRVITTCRASQSSVDYLNWYQKPKAPKLLIFDTSNLQSGVPS 57
 QY 58 QKPKAPKLLIYDTSNLASVGRVPSRFGSGSGTDYTLTISSLPEDFATYYCQOWSSYP-LTFGGGKVEIK 117
 Db 59 QKPKAPKLLIYAVSNLQVGVPSRFGSGSGTAEFTLTISLQPDFAFYCQSYTNPFTVFGGTTVDIK 118
 QY 118 TFGGKTKVEIK 128
 Db 119 TFGGKTKVDNK 129

RESULT 10
 ID KVIS_HUMAN STANDARD; PRT; 108 AA.
 AC P01611;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE IG KAPPA CHAIN V-I REGION WES.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]
 SEQUENCE-81092279; PubMed=6778806;
 Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
 "Preparative separation of the tryptic hydrolysate of a protein by
 RT high-pressure liquid chromatography. The primary structure of a
 RT monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein
 RT Wes).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC PIR: A01877; KIHUWS.
 DR HSP: P80362; IWT.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_v.
 DR SMART: SM00406; Ig; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 35 49 FRAMEWORK 2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 57 98 FRAMEWORK 3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 98 107 FRAMEWORK 4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60E45 CRC64;

Query Match 65.3%; Score 427.5; DB 1; Length 108;
 Best Local Similarity 77.6%; Pred. No. 1.7e-34;
 Matches 83; Conservative 12; Mismatches 11; Indels 1; Gaps 1;

QY 23 DIQMTQSPSSLSASVGRVITTCRASQSSVDYLNWYQKPKAPKLLIYDTSNLQSGVPS 81
 Db 1 DIQMTQSPSSLSASVGRVITTCRASQSSVDYLNWYQKPKAPKLLIYDTSNLQSGVPS 81
 QY 82 RFGSGSGTDYTLTISSLPEDFATYYCQOWSSYP-LTFGGGKVEIK 128
 Db 61 RFGSGSGTAEFTLTISLQPDFAFYCQSYTNPFTVFGGTTVDIK 107

RESULT 11
 ID KVIS_HUMAN STANDARD; PRT; 129 AA.
 AC P04431;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DE IG KAPPA CHAIN V-I REGION WALKER PRECURSOR.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]

SEQUENCE FROM N.A.
 MEDLINE=85014148; PubMed=6091049;
 Klobbeck H.G., Combriato G., Zachau H.G.;
 "Immunoglobulin genes of the kappa light chain type from two human
 lymphoid cell lines are closely related.";
 Nucleic Acids Res. 12:6995-7006(1984).
 CC -----

EMBL; X00966; CAA25478.1; ALT_TERM.
 DR PIR: A01884; KIHUJ.
 DR HSP: P80362; IWT.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_v.
 DR SMART: SM00406; Ig; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION DAUDI.
 FT DOMAIN 23 45 FRAMEWORK 1.
 FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 57 71 FRAMEWORK 2.
 FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 79 110 FRAMEWORK 3.
 FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 120 129 FRAMEWORK 4.
 FT DISULFID 45 110 BY SIMILARITY.
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 14235 MW; CAF076BC7E5574C8 CRC64;

Query Match 65.7%; Score 430.5; DB 1; Length 129;
 Best Local Similarity 69.5%; Pred. No. 1.1e-34;
 Matches 91; Conservative 12; Mismatches 23; Indels 5; Gaps 3;

QY 1 MDOFV--QIFSFLLISASVILSGDIQMTQSPSSLSASVGRVITTCRASQSSVDYLNWYQKPKAPKLLIFDTSNLQSGVPS 3;
 Db 1 MDMRPAQLGLLLWLRLV--KCDIQMTQSPSSLSASVGRVITTCRASQSSVDYLNWYQKPKAPKLLIFDTSNLQSGVPS 57
 QY 58 QKPKAPKLLIYDTSNLASVGRVPSRFGSGSGTDYTLTISSLPEDFATYYCQOWSSYP-LTFGGGKVEIK 117
 Db 59 QKPKAPKLLIYAVSNLQVGVPSRFGSGSGTAEFTLTISLQPDFAFYCQSYTNPFTVFGGTTVDIK 118
 QY 118 TFGGKTKVEIK 128
 Db 119 TFGGKTKVDNK 129

us-09-772-103-8.rsp

Mon Jul 1 16:28:15 2002

Gall W.E., Edelman G.M.;

"The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";

Biochemistry 9:3188-3196(1970).

-I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.

CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.

CC PIR; A01866; KIHUEU.

DR HSP; P01607; IREI.

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003596; Ig_V.

DR Pfam: PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR Immunoglobulin V region.

KW DOMAIN 1 23

FT DOMAIN 24 34

FT DOMAIN 35 49

FT DOMAIN 50 56

FT DOMAIN 57 88

FT DOMAIN 89 97

FT DOMAIN 98 107

FT DISULFID 23 88

FT NON_TER 108 108

SEQ SEQUENCE 108 AA; 9CD294F2F4D88823 CRC64;

Query Match 64.5%; Score 422.5; DB 1; Length 108;

Best Local Similarity 76.6%; Pred. No. 5.2e-34;

Matches 82; Conservative 13; Mismatches 11; Indels 1; Gaps 1;

QY 23 DIQMTQSPSSLSASVGRVTITCSATSI-TYMSWYQKPKAPKLLIYDTSNLASGVPS 81

Db 1 DIQMTQSPSSLSASVGRVTITCRASQINLWLAQKPKAPKLLMYKASSLESQVPS 60

QY 82 RFGSGSGDITLTITSSLPQDFATYTCQWSSYPLTFGGGKVEIK 128

Db 61 RFGSGSGDITLTITSSLPQDFATYTCQWSSYPLTFGGGKVEIK 107

RESULT 13

KVIM_HUMAN STANDARD; PRT; 108 AA.

AC P01605;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-I REGION LAY.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TaxID=9606;

OX [1]

RN SEQUENCE.

RP MEDLINE=77038198; PubMed=824717;

RX Capra J.D., Kiappner D.G.;

RA "Complete amino acid sequence of the variable domains of two human

IGM anti-gamma globulins (Lay/Pom) with shared idiotype

specificities.";

RL Scand. J. Immunol. 5:677-684(1976).

CC -I- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS

CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,

WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.

CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA

GLOBULIN ACTIVITY.

CC PIR; A01871; KIHULX.

DR HSP; P01607; IREI.

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003596; Ig_V.

DR Pfam: PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR Immunoglobulin V region.

KW DOMAIN 1 23

FT DOMAIN 24 34

FT DOMAIN 35 49

FT DISULFIDE BOND.

RP MEDLINE=71064023; PubMed=5489770;

RX Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;

RA "The covalent structure of a human gamma G-immunoglobulin. VI. Amino

acid sequence of the light chain.";

RL Biochemistry 9:3155-3161(1970).

RN [2]

RP DISULFIDE BOND.

RX MEDLINE=71064027; PubMed=4923144;

"Immunoglobulin genes of the kappa light chain type from two human lymphoid cell lines are closely related.";

Nucleic Acids Res. 12:6995-7006(1984).

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modified and this statement is not removed. Usage by and for commercial

entities requires a license agreement (see <http://www.isb-sib.ch/announce/>)

or send an email to license@isb-sib.ch.

CC EMBL; X00965; CAA25477.1; ALT_TERM.

DR PIR; A01883; KIHUNK.

DR HSP; P01607; IREI.

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003596; Ig_V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR Immunoglobulin V region; Signal.

KW SIGNAL 22

FT CHAIN 23 129

FT DOMAIN 23 45

FT DOMAIN 46 56

FT DOMAIN 57 71

FT DOMAIN 72 78

FT DOMAIN 79 110

FT DOMAIN 111 119

FT DOMAIN 120 129

FT DISULFID 45 110

FT NON_TER 129 129

SEQ SEQUENCE 129 AA; F941FA07D4AFC2F9 CRC64;

Query Match 65.3%; Score 427.5; DB 1; Length 129;

Best Local Similarity 70.2%; Pred. No. 2.1e-34;

Matches 92; Conservative 13; Mismatches 21; Indels 5; Gaps 3;

QY 1 MDFOV--QIFSTLLASVTLSDGIQMTQSPSSLSASVGRVTITCSATSI-TYMSWY 57

Db 1 MDNRVPAQLGLLLWLGR--ARCDIQTQSPSSLSASVGRVTITCRASQISINLWY 58

QY 58 QKPKGAPKLLIYDTSNLASGVPSRSGSGDITLTITSSLPQDFATYTCQWSSYPL 117

Db 59 QKPKGAPKLLIYAASLQSGVTSRFGSGSGDITLTITSSLPQDFATYTCQWSSYPL 118

QY 118 TFGGKVEIK 128

Db 119 TFGGKVEIK 129

RESULT 12

KVIF_HUMAN STANDARD; PRT; 108 AA.

AC P01598;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-I REGION EU.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TaxID=9606;

OX [1]

RN SEQUENCE.

RP MEDLINE=71064023; PubMed=5489770;

RX Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;

RA "The covalent structure of a human gamma G-immunoglobulin. VI. Amino

acid sequence of the light chain.";

RL Biochemistry 9:3155-3161(1970).

RN [2]

RP DISULFIDE BOND.

RX MEDLINE=71064027; PubMed=4923144;

```

db
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 RESSGAGTEFTLTSSLPDEFATYCLQNSYPRSGGKVEIK 107

```

RESULT	15
KVIR_HUMAN	
ID	KVIR_HUMAN
AC	STANDARD;
PRT	108 AA.
AD	P01610;
DT	21-JUL-1986 (Rel. 01, Created)
DDT	21-JUL-1986 (Rel. 01, Last sequence update)
DDT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	IG KAPPA CHAIN V-I REGION WEA.
DSE	Mus sapientis (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;	[1]
SEQUENCE	
RP	MEDLINE=83273707; PubMed=6410398;
Coor	

1. "Amino acid sequence of the Fv region of a human monoclonal IgM
 2. (protein WE4) with antibody activity against 3,4-pyruvylated
 3. galactose in Klebsiella polysaccharides K30 and K33.";
 4. Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841 (1983).
 5. -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
 6. AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
 7. WALDENSTROM'S S MACROGLOBULINEMIA.
 8. PIR; A01876; KIHUWE.
 9. HSP; P80362; LWTL.
 10. InterPro; IPR003006; Iq_MHC.
 11. InterPro; IPR003596; Iq_v.
 12. Pfam; PF00047; Iq; 1.
 13. SMART; SM00406; IGV; 1.
 14. Immunoglobulin v region; Monoclonal antibody.
 15. DOMAIN 1
 16. 23
 17. FRAMEWORK 1.
 18. 24 34
 19. COMPLEMENTARITY-DETERMINING 1.
 20. DOMAIN 35 49
 21. FRAMEWORK 2.
 22. 50 56
 23. COMPLEMENTARITY-DETERMINING 2.
 24. DOMAIN 57 88
 25. FRAMEWORK 3.
 26. 89 97
 27. COMPLEMENTARITY-DETERMINING 3.
 28. DOMAIN 98 107
 29. FRAMEWORK 4.
 30. DISULFID 23 88
 31. NON_TER 108 108
 32. BY SIMILARITY.
 33. SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRG64;

```

SEQUENCE      108 AA: 11840 MW: 9249B61F0945618C CRC64;

Query Match
Best Local Similarity      64.4%; Score 421.5; DB 1; Length 108;
Matches      82; Conservative 76.6%; Pred. No. 6.4e-34;
Indels      13; Mismatches 13; Gaps 1;

23 DLOMTQSPSSUSASVGDVRTITTCATSSI-TYMSYQQKPGKPKLLIYDTSNLASGVPS 81
|||||.....|.....|.....|.....|.....|.....|.....|.....|
1 DLOMTQSPSSUSASVGDVRTITTCRASQIRNDLTWYQQKPGTAPKRLIYATSIQSGVPS 60
|||||.....|.....|.....|.....|.....|.....|.....|.....|

82 RFSGSGGTDYTLTILSSLPQEDFATYYCCQWSSYPLTFGGGKVEIK 128
|||||.....|.....|.....|.....|.....|.....|.....|.....|
61 RFSGSGSGTEFTLINSLPQEDFATYYCYLQYSSFPWTFQGGTKVEVK 107
|||||.....|.....|.....|.....|.....|.....|.....|.....|

rch completed: May 7, 2002, 12:08:53
time: 451 sec

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rch completed: May  7, 2002, 12:08:53
time: 451 sec
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